

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 8, 2002, 22:02:08 ; Search time 4414.95 Seconds
(without alignments)
10683.793 Million cell updates/sec

Title: PCT-US01-46559-1
Perfect score: 2254
Sequence: 1 ctcgctctctctctacttgg.....tttgaaaaa.....2254

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg.hum.*
- 31: em.htg_inv.*
- 32: em.htg_other.*
- 33: em.htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description

1	1652.4	73.3	1880	6	AX017982
2	1330	59.0	1330	6	AX017833
3	1160.4	51.5	1162	9	BC000848
4	1115.4	49.5	2523	9	AK056388
5	969.4	43.0	992	9	BC009286
6	880.8	39.1	885	9	HS2423666
7	772	34.3	772	9	BC015316
8	557	24.7	2939	9	BC017708
9	488.4	21.7	2939	9	AL592078
10	461.2	20.5	2993	9	AK000617
11	422.6	18.7	5281	9	HS008191
12	406	18.0	61087	2	AC102392
13	371.4	16.5	585	9	AF397158
14	371.4	16.5	2235	9	HUMRGEA
15	371.4	16.5	25606	2	AC010554
16	371.4	16.5	42999	9	HS013369
17	371.4	16.5	43962	2	AC068192
18	371.4	16.5	61490	2	AC025630
19	371.4	16.5	101641	2	AL158197
20	371.4	16.5	112833	2	AC068881
21	371.4	16.5	136630	2	AC023572
22	371.4	16.5	140653	2	AL355134
23	371.4	16.5	150286	2	AL353644
24	369.8	16.4	1869	6	AX205305
25	369.8	16.4	1869	6	AX207387
26	369.8	16.4	1869	6	HSRRN18S
27	368.8	16.4	50872	2	AC084140
28	368.2	16.3	1969	9	HUMRGE
29	368.2	16.3	55939	2	AC091017
30	367	16.3	61490	2	AC025630
31	363.4	16.1	1824	4	DNA311674
32	363.4	16.1	1824	4	ECA311673
33	360.6	16.0	183292	2	AC094121
34	355.6	15.8	1825	4	EU311675
35	345	15.3	21908	2	AC091632
36	343.4	15.2	2062	10	MMETS82
37	342.4	15.2	39133	2	AC105701
38	342.4	15.2	214755	2	AC091339
39	338.6	15.0	918	10	MUSRGE51
40	333	14.8	1920	10	RATRGEA
41	331.4	14.7	1869	6	AX205304
42	331.4	14.7	1869	6	AX207386
43	331.4	14.7	1869	6	MMRNA18
44	331.4	14.7	22118	10	MM458RRA
45	330.4	14.7	1874	10	RNRRNA06

ALIGNMENTS

RESULT	AX017982	1880 bp	DNA	linear	PAT 07-SEP-2000
LOCUS	AX017982	Sequence 217 from Patent WO9946375.			
DEFINITION	AX017982				
ACCESSION	AX017982.1	GI:10042481			
VERSION					
KEYWORDS	human.				
SOURCE	Homo sapiens				
ORGANISM					

Human nucleic acid sequences from prostate tissue
Patent: WO 9946375-A 217 16-SEP-1999.
SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN
(DE); PILARSKY CHRISTIAN (DE)
Location/Qualifiers
1..1880
/organism="Homo sapiens"
/db_xref="taxon:9606"

